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Sequence Listing was accepted.

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Reviewer: Keisha Douglas

Timestamp: [year=2008; month=9; day=9; hr=13; min=59; sec=30; ms=527; ]

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Application No: 10584225 Version No: 1.0

Input Set:

Output Set:

Started: 2008-08-07 13:52:17.767  
Finished: 2008-08-07 13:52:18.541  
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 774 ms  
Total Warnings: 9  
Total Errors: 0  
No. of SeqIDs Defined: 10  
Actual SeqID Count: 10

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
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W 213	Artificial or Unknown found in <213> in SEQ ID (5)
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W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)

# SEQUENCE LISTING

<110> YANG, DAICHANG  
HENNEGAN, KEVIN  
HUANG, NING

<120> METHODS OF EXPRESSING HETEROLOGOUS PROTEIN IN PLANT  
SEEDS USING MONOCOT NON SEED-STORAGE PROTEIN PROMOTERS

<130> 023231-00033

<140> 10584225

<141> 2008-08-07

<150> PCT/US03/39107

<151> 2003-12-23

<160> 10

<170> PatentIn Ver. 3.3

<210> 1

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
primer

<400> 1

gggaatattg taccagccgc caacttctga

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<210> 2

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
primer

<400> 2

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33

<210> 3

<211> 393

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polynucleotide

<400> 3

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cgcgcaacca actacaacgc cggcgaccgc tccaccgact acggcatctt ccagatcaac 180
tcccgtact ggtgcaacga cggcaagacg cccggggcgc tcaacgcctg ccacctctcc 240
tgctcggccc tgctgcaaga caacatcgcc gacgccgtcg cgtgcgcgaa gcgcgtcgtc 300
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gtgcgccagt acgtccaggg ctgcggcgtc tga 393
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<210> 4

<211> 714

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polynucleotide

<400> 4

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caaagtttgc attctccact gacataatgc aaaataagat atcatcgatg acatagcaac 180
tcatgcatca tatcatgcct ctctcaacct attcattcct actcatctac ataagtatct 240
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ctatatgtca tattgcaaaa agaggagagc ttataagaca aggcattgact cacaaaaatt 420
cacttgccct tctgtgcaaa aagaggaggg ctttacatta tccatgtcat attgcaaaag 480
aaagagagaa agaacaacac aatgctgctg caattataca tatctgtatg tccatcatta 540
ttcatccacc tttcgtgtac cacacttcat atatcataag agtcacttca cgtctggaca 600
ttaacaaact ctatcttaac atttagatgc aagagccttt atctcactat aaatgcacga 660
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<210> 5

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polynucleotide

<400> 5

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ggctccctag cc 72
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<210> 6

<211> 919

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polynucleotide

<400> 6

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catagcataa cccacctggc gatcctctcc ttgtcacctc gtgagagagc gaacaccggg 180
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gaactaagta gcaacatgta aggagtcagt tttcgagata ccacacaaca ccaattttcc 360
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gtttggatcc ttcttcaaca atttcacac actacaaggc cagttcaca aagcttaaag 660
cgtgagcatt ggtacaaaac tagttgtggt ctatcttgag aaaagggaac acttagtaca 720
cgaaacgtca cctgtctcaa caacttgcac catctctgtt ggctcgcaa gtaactttat 780
ttagtatacc aacttaattt gtgagcatta gccaaagcaa cacacaatgg taggcaaaaa 840
ccatgtcact aagcaataaa taaaggggag cctcaacca tctattcatc tccaccacca 900
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<210> 7

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
polynucleotide

<400> 7

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tactcagaag ctggcggtg gtacaat 87
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<210> 8

<211> 11

<212> PRT

<213> Homo sapiens

<400> 8

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1           5           10
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<210> 9

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
peptide

<400> 9

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Lys Val Phe Glu Arg Glu Leu Ala Arg Thr
1           5           10
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<210> 10  
<211> 130  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
polypeptide

<400> 10  
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1 5 10 15  
Met Asp Gly Tyr Arg Gly Ile Ser Leu Ala Asn Trp Met Cys Leu Ala  
20 25 30  
Lys Trp Glu Ser Gly Tyr Asn Thr Arg Ala Thr Asn Tyr Asn Ala Gly  
35 40 45  
Asp Arg Ser Thr Asp Tyr Gly Ile Phe Gln Ile Asn Ser Arg Tyr Trp  
50 55 60  
Cys Asn Asp Gly Lys Thr Pro Gly Ala Val Asn Ala Cys His Leu Ser  
65 70 75 80  
Cys Ser Ala Leu Leu Gln Asp Asn Ile Ala Asp Ala Val Ala Cys Ala  
85 90 95  
Lys Arg Val Val Arg Asp Pro Gln Gly Ile Arg Ala Trp Val Ala Trp  
100 105 110  
Arg Asn Arg Cys Gln Asn Arg Asp Val Arg Gln Tyr Val Gln Gly Cys  
115 120 125  
Gly Val  
130